

# SEQUENCE LISTING

<110> KIM, Young Tae  
LEE, Jae Hyung

<120> Gene involved in the biosynthesis of carotenoid and marine microorganism, paracoccus haeundaesis, producing the carotenoid

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<141> 2006-06-05

<150> PCT/KR2004/000752  
<151> 2003-03-31

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 Ile Leu Ile Glu Asp Thr Arg Tyr Ser Asp Gly Gly Asn Leu Asp Asp  
 195 200 205  
 Asp Ala Leu Ala Ala Ala Ser His Asp Tyr Ala Arg Gln Gln Gly Trp  
 210 215 220  
 Thr Gly Ala Glu Val Arg Arg Glu Arg Gly Ile Leu Pro Ile Ala Leu  
 225 230 235 240  
 Ala His Asp Ala Ala Gly Phe Trp Ala Asp His Ala Glu Gly Pro Val  
 245 250 255  
 Pro Val Gly Leu Arg Ala Gly Phe Phe His Pro Val Thr Gly Tyr Ser  
 260 265 270  
 Leu Pro Tyr Ala Ala Gln Val Ala Asp Val Val Ala Gly Leu Ser Gly  
 275 280 285  
 Pro Pro Gly Thr Asp Ala Leu Arg Gly Ala Ile Arg Asp Tyr Ala Ile  
 290 295 300  
 Asp Arg Ala Arg Arg Asp Arg Phe Leu Arg Leu Leu Asn Arg Met Leu  
 305 310 315 320  
 Phe Arg Gly Cys Ala Pro Asp Arg Arg Tyr Thr Leu Leu Gln Arg Phe  
 325 330 335  
 Tyr Arg Met Pro His Gly Leu Ile Glu Arg Phe Tyr Ala Gly Arg Leu  
 340 345 350  
 Ser Val Ala Asp Gln Leu Arg Ile Val Thr Gly Lys Pro Pro Ile Pro  
 355 360 365  
 Leu Gly Thr Ala Ile Arg Cys Leu Pro Glu Arg Pro Leu Leu Lys Glu  
 370 375 380  
 Asn Ala  
 385

<210> 11  
 <211> 1506  
 <212> DNA  
 <213> *Paracoccus haeundaesis*

<220>  
 <223> crtI gene

<400> 11  
 atgaacgccc attcgccgc ggccaagacc gccatcgtga tcggcgcagg ctttggcggg 60  
 ctggccctgg ccatacgcct gcagtcgcgc ggcatacgca ccacctggt cgaggcccg 120  
 gacaagcccg gcgggcgcgc ctatgtctgg cacgatcagg gccatgtctt cgacgcgggc 180  
 ccgaccgtca tcaccgacc cgatgcgctc aaggagctgt gggcgtgac cgggcaggac 240  
 atggcgcgcg acgtgacgt gatgccggtg tcgcccttct atcgactgat gtggccgggc 300  
 gggaaaggtct tcgattacgt gaacgaggcc gatcagctgg agcgccagat cgcccagttc 360  
 aaccggacg acctggaagg ataccgccc ttccgtgatt acgcgaggga ggtgtatcag 420  
 gagggctacg tcaagctggg caccgtgcc ttctcaagc tgggccagat gctcaaggcc 480  
 gcgcccgcgc tgatgaagct ggaggcctat aagtccgtcc atgccaaggt cgcgaccttc 540  
 atcaaggacc cctatctgcg gcaggcggtt tcgtatcaca cgctgctggt gggcgggaat 600  
 cccttctcga ccagctcgat ctatgcgctg atccacgcgc tggagcggcg cggcggggtc 660  
 tggttcgcca agggcggcac caaccagctg gtcgcgggca tggtcgcgct gttcgaacgg 720  
 cttggcggcc agatgatgct gaacgccaa gtcgcccga tcgagaccga gggcgcgcgcg 780  
 accacgggcg tcacctggc ggacgggcgc tctttaagg cgcacatggt cgccagcaac 840  
 ggcgacgtca tgcacaacta tcgcgacctg ctgggccaca cggcccgcgg gcagagccgc 900  
 gcgaaatcgc tggaccgcaa gcgctggtcc atgtcgttgt tcgtgctgca tttcggtctg 960  
 cgcgaggcgc ccaaggacat cgcgcatcac accatcctgt tcggccccc ctacaggag 1020  
 ctggtcaacg agatcttcaa gggcccgaag ctggccgagg atttctcgt gtacctgcat 1080  
 tcgccctgca cgaccgatcc ggacatggcg cctccgggca tgtccacgca ttacgtgctg 1140  
 gccccgtgc cgcactcggg ccgcgccgag atcgattggg cggtcgaggg gccgcgctat 1200  
 gccgaccgca tcctggcgtc cctggaggag cggctgatcc cgaacctgcg cgccaacctg 1260  
 accacgacgc gcactttcac gccgcggat ttccgcagcg aactgaacgc ccatacggc 1320  
 agcgccttct cggtcgagcc gatcctgacg caatccgcgt ggttccggcc gcacaaccgc 1380

gacaagacga tccgcaactt ctatctggtc ggcgcgggca cccatccggg cgcgggcatt 1440  
 ccgggcgtcg tgggctcggc caaggccacg gccaggtga tgctgtccga cctggcgggc 1500  
 gcatga 1506

<210> 12  
 <211> 501  
 <212> PRT  
 <213> Paracoccus haeundaesis

<220>  
 <223> crtI amino acid

<400> 12  
 Met Asn Ala His Ser Pro Ala Ala Lys Thr Ala Ile Val Ile Gly Ala  
 1 5 10 15  
 Gly Phe Gly Gly Leu Ala Leu Ala Ile Arg Leu Gln Ser Ala Gly Ile  
 20 25 30  
 Ala Thr Thr Leu Val Glu Ala Arg Asp Lys Pro Gly Gly Arg Ala Tyr  
 35 40 45  
 Val Trp His Asp Gln Gly His Val Phe Asp Ala Gly Pro Thr Val Ile  
 50 55 60  
 Thr Asp Pro Asp Ala Leu Lys Glu Leu Trp Ala Leu Thr Gly Gln Asp  
 65 70 75 80  
 Met Ala Arg Asp Val Thr Leu Met Pro Val Ser Pro Phe Tyr Arg Leu  
 85 90 95  
 Met Trp Pro Gly Gly Lys Val Phe Asp Tyr Val Asn Glu Ala Asp Gln  
 100 105 110  
 Leu Glu Arg Gln Ile Ala Gln Phe Asn Pro Asp Asp Leu Glu Gly Tyr  
 115 120 125  
 Arg Arg Phe Arg Asp Tyr Ala Glu Glu Val Tyr Gln Glu Gly Tyr Val  
 130 135 140  
 Lys Leu Gly Thr Val Pro Phe Leu Lys Leu Gly Gln Met Leu Lys Ala  
 145 150 155 160  
 Ala Pro Ala Leu Met Lys Leu Glu Ala Tyr Lys Ser Val His Ala Lys  
 165 170 175  
 Val Ala Thr Phe Ile Lys Asp Pro Tyr Leu Arg Gln Ala Phe Ser Tyr  
 180 185 190  
 His Thr Leu Leu Val Gly Gly Asn Pro Phe Ser Thr Ser Ser Ile Tyr  
 195 200 205  
 Ala Leu Ile His Ala Leu Glu Arg Arg Gly Gly Val Trp Phe Ala Lys  
 210 215 220

Gly Gly Thr Asn Gln Leu Val Ala Gly Met Val Ala Leu Phe Glu Arg  
 225 230 235 240  
 Leu Gly Gly Gln Met Met Leu Asn Ala Lys Val Ala Arg Ile Glu Thr  
 245 250 255  
 Glu Gly Ala Arg Thr Thr Gly Val Thr Leu Ala Asp Gly Arg Ser Leu  
 260 265 270  
 Arg Ala Asp Met Val Ala Ser Asn Gly Asp Val Met His Asn Tyr Arg  
 275 280 285  
 Asp Leu Leu Gly His Thr Ala Arg Gly Gln Ser Arg Ala Lys Ser Leu  
 290 295 300  
 Asp Arg Lys Arg Trp Ser Met Ser Leu Phe Val Leu His Phe Gly Leu  
 305 310 315 320  
 Arg Glu Ala Pro Lys Asp Ile Ala His His Thr Ile Leu Phe Gly Pro  
 325 330 335  
 Arg Tyr Arg Glu Leu Val Asn Glu Ile Phe Lys Gly Pro Lys Leu Ala  
 340 345 350  
 Glu Asp Phe Ser Leu Tyr Leu His Ser Pro Cys Thr Thr Asp Pro Asp  
 355 360 365  
 Met Ala Pro Pro Gly Met Ser Thr His Tyr Val Leu Ala Pro Val Pro  
 370 375 380  
 His Leu Gly Arg Ala Glu Ile Asp Trp Ala Val Glu Gly Pro Arg Tyr  
 385 390 395 400  
 Ala Asp Arg Ile Leu Ala Ser Leu Glu Glu Arg Leu Ile Pro Asn Leu  
 405 410 415  
 Arg Ala Asn Leu Thr Thr Thr Arg Ile Phe Thr Pro Ala Asp Phe Ala  
 420 425 430  
 Ser Glu Leu Asn Ala His His Gly Ser Ala Phe Ser Val Glu Pro Ile  
 435 440 445  
 Leu Thr Gln Ser Ala Trp Phe Arg Pro His Asn Arg Asp Lys Thr Ile  
 450 455 460  
 Arg Asn Phe Tyr Leu Val Gly Ala Gly Thr His Pro Gly Ala Gly Ile  
 465 470 475 480  
 Pro Gly Val Val Gly Ser Ala Lys Ala Thr Ala Gln Val Met Leu Ser  
 485 490 495  
 Asp Leu Ala Gly Ala  
 500

<210> 13  
 <211> 915  
 <212> DNA  
 <213> Paracoccus haeundaesis

<220>  
 <223> crtB gene

<400> 13  
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 acggcggcca agctgatgcc gccgggcacg cgcgacgaca cggatgatgct ctatgcctgg 120  
 tgccgccacg cggatgacgt gatcgacggg caggccctgg gcagccgccc cgaggcgggtg 180  
 aacgacccgc aggcgcgggt ggacggcctg cgcgtcgaca cgctggcggc cctgcagggc 240  
 gacgggtccg tgaccccgcc ctttgccgcg ctgcgcgcgg tggcgcggcg gcatgatttc 300  
 ccgcaggcct ggcccatgga cctgatcgaa ggcttcgcga tggatgtcga ggcgcgcgac 360  
 tatcgacgc tggatgacgt gctggaatat tctatcacg tcgcaggcat cgtcggcgtg 420  
 atgatggccc gcgtgatggg cgtgcgcgac gatcctgtcc tggaccgcgc ctgcgacctg 480  
 gggctggcgt tccagctgac caacatcgcg cgcgacgtga tcgacgatgc gcgcatcggg 540  
 cgggtgctatc tgccggggga ctggctggac caggcggggc cgcggatcga cgggccgggtg 600  
 ccgtcgccgg agctgtacac agtgatcctc cggctgttgg atgaggcgga accctattac 660  
 gcgtcggcgc ggggtgggtct ggcggatctg ccaccgcgct gcgcctggtc catcgccgcc 720  
 gcgctacgga tctatcgcg catcgggctg cgcacccgca agagcggggc gcaggcctat 780  
 cgccagcgga tcagcacgtc caaggctgcc aagatcggcc tgctgggcgt cgggggctgg 840  
 gatgtcgcgc gatcacgcct gccggggggc ggcgtgtcgc ggcagggcct ctggaccggg 900  
 ccgcatcacg tctag 915

<210> 14  
 <211> 304  
 <212> PRT  
 <213> Paracoccus haeundaesis

<220>  
 <223> crtB amino acid

<400> 14  
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 Gln Ser Phe Ala Thr Ala Ala Lys Leu Met Pro Pro Gly Ile Arg Asp  
 20 25 30

Asp Thr Val Met Leu Tyr Ala Trp Cys Arg His Ala Asp Asp Val Ile  
           35                          40                          45  
 Asp Gly Gln Ala Leu Gly Ser Arg Pro Glu Ala Val Asn Asp Pro Gln  
           50                          55                          60  
 Ala Arg Leu Asp Gly Leu Arg Val Asp Thr Leu Ala Ala Leu Gln Gly  
           65                          70                          75                          80  
 Asp Gly Pro Val Thr Pro Pro Phe Ala Ala Leu Arg Ala Val Ala Arg  
                           85                          90                          95  
 Arg His Asp Phe Pro Gln Ala Trp Pro Met Asp Leu Ile Glu Gly Phe  
                   100                          105                          110  
 Ala Met Asp Val Glu Ala Arg Asp Tyr Arg Thr Leu Asp Asp Val Leu  
           115                          120                          125  
 Glu Tyr Ser Tyr His Val Ala Gly Ile Val Gly Val Met Met Ala Arg  
           130                          135                          140  
 Val Met Gly Val Arg Asp Asp Pro Val Leu Asp Arg Ala Cys Asp Leu  
           145                          150                          155                          160  
 Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp Val Ile Asp Asp  
                           165                          170                          175  
 Ala Arg Ile Gly Arg Cys Tyr Leu Pro Gly Asp Trp Leu Asp Gln Ala  
                   180                          185                          190  
 Gly Ala Arg Ile Asp Gly Pro Val Pro Ser Pro Glu Leu Tyr Thr Val  
           195                          200                          205  
 Ile Leu Arg Leu Leu Asp Glu Ala Glu Pro Tyr Tyr Ala Ser Ala Arg  
           210                          215                          220  
 Val Gly Leu Ala Asp Leu Pro Pro Arg Cys Ala Trp Ser Ile Ala Ala  
           225                          230                          235                          240  
 Ala Leu Arg Ile Tyr Arg Ala Ile Gly Leu Arg Ile Arg Lys Ser Gly  
                           245                          250                          255  
 Pro Gln Ala Tyr Arg Gln Arg Ile Ser Thr Ser Lys Ala Ala Lys Ile  
           260                          265                          270  
 Gly Leu Leu Gly Val Gly Gly Trp Asp Val Ala Arg Ser Arg Leu Pro  
           275                          280                          285  
 Gly Ala Gly Val Ser Arg Gln Gly Leu Trp Thr Arg Pro His His Val  
           290                          295                          300

<210> 15  
 <211> 882  
 <212> DNA

<213> Paracoccus haeundaesis

<220>

<223> crtE gene

<400> 15

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gccagggat tcggtgccgt gtcgcagccg ctccggcgcg ccatgagcca tggcgcgctg 120
tcgtcgggca ggcgggtccg cggcatgctg atgctgcttg cggcagaggc ctccggcggg 180
gtctgcgaca cgatcgtcga cggcgccctgc gcggtcgaga tggatcatgc cgcacgctg 240
atcttcgacg acctgccctg catggacgat gccgggctgc gcccgggccg gcccgcgacc 300
catgtggcgc atggcgaaag ccgtgccgtg ctggggcgga tcgccctgat caccgaggca 360
atggccctgc tggccgggtg gcgcggcgcg tcgggcacgg tcggggcgca gctggtgcgg 420
atcctgtcgc ggtccctggg gccgcagggc ctgtgcgccg gccaggacct ggacctgcac 480
gcggccaaga acggcgcggg ggtcgaacag gaacaggacc tgaagaccgg cgtgctgttc 540
atcgccgggc tggagatgct ggccgtgacg aaggagtctg acgccgagga gcagaccag 600
atgatcgact ttggccgtca gctgggccgc gtgttccagt cctatgacga cctgctggac 660
gtcgtgggcg accaggcggc gcttggcaag gataccggtc gcgatgccgc ggccccggc 720
ccgcggcgcg gccttctggc cgtgtcagac ctgcagaacg tgtcccgta ttacgaggcc 780
agccgcgccc aactggacgc gatgctgcgc agcaagcgcc ttcaggctcc ggaaatcgcg 840
gcctgtctgg aacgggttct gccctacgcc gcgcgcgcct ag 882
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<210> 16

<211> 293

<212> PRT

<213> Paracoccus haeundaesis

<220>

<223> crtE amino acid

<400> 16

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Met Arg Arg Asp Val Asn Pro Ile His Ala Thr Leu Leu Gln Thr Arg
 1             5             10             15
Leu Glu Glu Ile Ala Gln Gly Phe Gly Ala Val Ser Gln Pro Leu Gly
 20             25             30
Ala Ala Met Ser His Gly Ala Leu Ser Ser Gly Arg Arg Phe Arg Gly
 35             40             45
Met Leu Met Leu Leu Ala Ala Glu Ala Ser Gly Gly Val Cys Asp Thr
 50             55             60
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Ile Val Asp Ala Ala Cys Ala Val Glu Met Val His Ala Ala Ser Leu  
 65 70 75 80  
 Ile Phe Asp Asp Leu Pro Cys Met Asp Asp Ala Gly Leu Arg Arg Gly  
 85 90 95  
 Arg Pro Ala Thr His Val Ala His Gly Glu Ser Arg Ala Val Leu Gly  
 100 105 110  
 Gly Ile Ala Leu Ile Thr Glu Ala Met Ala Leu Leu Ala Gly Ala Arg  
 115 120 125  
 Gly Ala Ser Gly Thr Val Arg Ala Gln Leu Val Arg Ile Leu Ser Arg  
 130 135 140  
 Ser Leu Gly Pro Gln Gly Leu Cys Ala Gly Gln Asp Leu Asp Leu His  
 145 150 155 160  
 Ala Ala Lys Asn Gly Ala Gly Val Glu Gln Glu Gln Asp Leu Lys Thr  
 165 170 175  
 Gly Val Leu Phe Ile Ala Gly Leu Glu Met Leu Ala Val Ile Lys Glu  
 180 185 190  
 Phe Asp Ala Glu Glu Gln Thr Gln Met Ile Asp Phe Gly Arg Gln Leu  
 195 200 205  
 Gly Arg Val Phe Gln Ser Tyr Asp Asp Leu Leu Asp Val Val Gly Asp  
 210 215 220  
 Gln Ala Ala Leu Gly Lys Asp Thr Gly Arg Asp Ala Ala Ala Pro Gly  
 225 230 235 240  
 Pro Arg Arg Gly Leu Leu Ala Val Ser Asp Leu Gln Asn Val Ser Arg  
 245 250 255  
 His Tyr Glu Ala Ser Arg Ala Gln Leu Asp Ala Met Leu Arg Ser Lys  
 260 265 270  
 Arg Leu Gln Ala Pro Glu Ile Ala Ala Leu Leu Glu Arg Val Leu Pro  
 275 280 285  
 Tyr Ala Ala Arg Ala  
 290

<210> 17  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> forward primer for crt gene  
  
 <400> 17

gttccacgac tggggcatc

19

<210> 18

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse primer for crt gene

<400> 18

tccactgacc ttgttgaca aattgccg

28